SEQUENCE LISTING

<110> Kennedy, Giulia C.

<120> Polynucleotides Differentially Expressed
  in Adenocarcinomas, Polypeptides Encoded Thereby, and
  Methods of Use Thereof

<130> 2300-1575

<150> 60/145,612
<151> 1999-07-26

<150> 60/148,936
<151> 1999-08-13

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4612
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (698)...(3862)

<400> 1
```
atagcacgac tgtgtatgct ctggaggact gaaaggctgt acaagcccta tgtatttttt      60
ttcaaatata catatgcatg ggtcttgctg ctgcctcttt tgctgactgt aattggactt     120
tgaagcttcg aagttatatc ataaaaattt gtaacctttg tctgagagag agctcagcta     180
agcaatcact ttccacttct tttcacagga taatataaac gttttcttga aagcttgtga     240
acagattgga ttgaaagaag cccagctttt ccatcctgga gatctacagg attatcaaa      300
tcgagtcact gtcaagcaag aagagactga caggagagtg aaaaatgttt tgataacatt     360
gtactggctg ggaagaaaag cacaaagcaa cccgtactat aatggtcccc atcttaattt     420
gaaagcgttt gagaatcttt taggacaagc actgacgaag gcactcgaag actccagctt     480
cctgaaaaga agtggcaggg acagtggcta cggtgacatc tggtgtcctg aacgtggaga     540
atttcttgct cctccaaggc accataagag agaagattcc tttgaaagct tggactcttt     600
gggctcgagg tcattgacaa gctgctcctc tgatatcacg ttgagagggg ggcgtgaagg     660
ttttgaaagt gacacagatt cggaatttac attcaag atg cag gat tat aat aaa     715
                                          Met Gln Asp Tyr Asn Lys
                                          1                   5

gat gat atg tcg tat cga agg att tcg gct gtt gag cca aag act gcg     763
Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu Pro Lys Thr Ala
            10                  15                  20

tta ccc ttc aat cgt ttt tta ccc aac aaa agt aga cag cca tcc tat     811
```

-1-

```
Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg Gln Pro Ser Tyr
        25                  30                  35

gta cca gca cct ctg aga aag aaa aag cca gac aaa cat gag gat aac    859
Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys His Glu Asp Asn
        40                  45                  50

aga aga agt tgg gca agc ccg gtt tat aca gaa gca gat gga aca ttt    907
Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala Asp Gly Thr Phe
 55                  60                  65                  70

tca agg agt aag tcc atg agt gat gtc agc gca gaa gat gtt caa aac    955
Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu Asp Val Gln Asn
                75                  80                  85

ttg cgt cag ctg cgt tac gag gag atg cag aaa ata aaa tca caa tta   1003
Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile Lys Ser Gln Leu
                90                  95                  100

aaa gaa caa gat cag aaa tgg cag gat gac ctt gca aaa tgg aaa gat   1051
Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp
            105                 110                 115

cgt cga aaa agt tac act tca gat ctg cag aag aaa aaa gaa gag aga   1099
Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys Lys Lys Glu Glu Arg
        120                 125                 130

gaa gaa att gaa aag cag gca ctt gag aag tct aag aga agc tct aag   1147
Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys
135                 140                 145                 150

acg ttt aag gaa atg ctg cag gac agg gaa tcc caa aat caa aag tct   1195
Thr Phe Lys Glu Met Leu Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser
                155                 160                 165

aca gtt ccg tca aga agg aga atg tat tct ttt gat gat gtg ctg gag   1243
Thr Val Pro Ser Arg Arg Arg Met Tyr Ser Phe Asp Asp Val Leu Glu
            170                 175                 180

gaa gga aag cga ccc cct aca atg act gtg tca gaa gca agt tac cag   1291
Glu Gly Lys Arg Pro Pro Thr Met Thr Val Ser Glu Ala Ser Tyr Gln
            185                 190                 195

agt gag aga gta gaa gag aag gga gca act tat cct tca gaa att ccc   1339
Ser Glu Arg Val Glu Glu Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro
        200                 205                 210

aaa gaa gat tct acc act ttt gca aaa aga gag gac cgt gta aca act   1387
Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg Glu Asp Arg Val Thr Thr
215                 220                 225                 230
```

```
gaa att cag ctt cct tct caa agt cct gtg gaa gaa caa agc cca gcc        1435
Glu Ile Gln Leu Pro Ser Gln Ser Pro Val Glu Glu Gln Ser Pro Ala
            235             240             245

tct ttg tct tct ctg cgt tca cgg agc aca caa atg gaa tca act cgt        1483
Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr Gln Met Glu Ser Thr Arg
            250             255             260

gtt tca gct tct ctc ccc aga agt tac cgg aaa act gat aca gtc agg        1531
Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg
            265             270             275

tta aca tct gtg gtc aca cca aga ccc ttt ggc tct cag aca agg gga        1579
Leu Thr Ser Val Val Thr Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly
            280             285             290

atc tca tca ctc ccc aga tct tac acg atg gat gat gct tgg aag tat        1627
Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr
295             300             305             310

aat gga gat gtt gaa gac att aag aga act cca aac aat gtg gtc agc        1675
Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro Asn Asn Val Val Ser
            315             320             325

acc cct gca cca agc ccg gac gca agc caa ctg gct tca agc tta tct        1723
Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser
            330             335             340

agc cag aaa gag gta gca gca aca gaa gaa gat gtg aca agg ctg ccc        1771
Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp Val Thr Arg Leu Pro
            345             350             355

tct cct aca tcc ccc ttc tca tct ctt tcc caa gac cag gct gcc act        1819
Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr
            360             365             370

tct aaa gcc aca ttg tct tcc aca tct ggt ctt gat tta atg tct gaa        1867
Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu Asp Leu Met Ser Glu
375             380             385             390

tct gga gaa ggg gaa atc tcc cca caa aga gaa gtc tca aga tcc cag        1915
Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu Val Ser Arg Ser Gln
            395             400             405

gat cag ttc agt gat atg aga atc agc ata aac cag acg cct ggg aag        1963
Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys
            410             415             420

agt ctt gac ttt ggg ttt aca ata aaa tgg gat att cct ggg atc ttc        2011
Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe
            425             430             435
```

```
gta gca tca gtt gaa gca ggt agc cca gca gaa ttt tct cag cta caa    2059
Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln
    440             445             450

gta gat gat gaa att att gct att aac aac acc aag ttt tca tat aac    2107
Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn
455             460             465             470

gat tca aaa gag tgg gag gaa gcc atg gct aag gct caa gaa act gga    2155
Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly
            475             480             485

cac cta gtg atg gat gtg agg cgc tat gga aag gct ggt tca cct gaa    2203
His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu
            490             495             500

aca aag tgg att gat gca act tct gga att tac aac tca gaa aaa tct    2251
Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser
        505             510             515

tca aat cta tct gta aca act gat ttc tcc gaa agc ctt cag agt tct    2299
Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser
    520             525             530

aat att gaa tcc aaa gaa atc aat gga att cat gat gaa agc aat gct    2347
Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His Asp Glu Ser Asn Ala
535             540             545             550

ttt gaa tca aaa gca tct gaa tcc att tct ttg aaa aac tta aaa agg    2395
Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg
            555             560             565

cga tca caa ttt ttt gaa caa gga agc tct gat tcg gtg gtt cct gat    2443
Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp Ser Val Val Pro Asp
        570             575             580

ctt cca gtt cca acc atc agt gcc ccg agt cgc tgg gtg tgg gat caa    2491
Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg Trp Val Trp Asp Gln
        585             590             595

gag gag gag cgg aag cgg cag gag agg tgg cag aag gag cag gac cgc    2539
Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg
    600             605             610

cta ctg cag gaa aaa tat caa cgt gag cag gag aaa ctg agg gaa gag    2587
Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu Lys Leu Arg Glu Glu
615             620             625             630

tgg caa agg gcc aaa cag gag gca gag aga gag aat tcc aag tac ttg    2635
Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu
```

-4-

```
gat gag gaa ctg atg gtc cta agc tca aac agc atg tct ctg acc aca     2683
Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser Met Ser Leu Thr Thr
            650                 655                 660


cgg gag ccc tct ctt gcc acc tgg gaa gct acc tgg agt gaa ggg tcc     2731
Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser
            665                 670                 675


aag tct tca gac aga gaa gga acc cga gca gga gaa gag gag agg aga     2779
Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly Glu Glu Glu Arg Arg
        680                 685                 690


cag cca caa gag gaa gtt gtt cat gag gac caa gga aag aag ccg cag     2827
Gln Pro Gln Glu Glu Val Val His Glu Asp Gln Gly Lys Lys Pro Gln
695                 700                 705                 710


gat cag ctt gtt att gag aga gag agg aaa tgg gag caa cag ctt cag     2875
Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln
                715                 720                 725


gaa gag caa gag caa aag cgg ctt cag gct gag gct gag gag cag aag     2923
Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys
            730                 735                 740


cgt cct gcg gag gag cag aag cgc cag gca gag ata gag cgg gaa aca     2971
Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr
            745                 750                 755


tca gtc aga ata tac cag tac agg agg cct gtt gat tcc tat gat ata     3019
Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile
        760                 765                 770


cca aag aca gaa gaa gca tct tca ggt ttt ctt cct ggt gac agg aat     3067
Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn
775                 780                 785                 790


aaa tcc aga tct act act gaa ctg gat gat tac tcc aca aat aaa aat     3115
Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn
                795                 800                 805


gga aac aat aaa tat tta gac caa att ggg aac acg acc tct tca cag     3163
Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln
            810                 815                 820


agg aga tcc aag aaa gaa caa gta cca tca gga gca gaa ttg gag agg     3211
Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly Ala Glu Leu Glu Arg
            825                 830                 835


caa caa atc ctt cag gaa atg agg aag aga aca ccc ctt cac aat gac     3259
```

-5-

```
Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr Pro Leu His Asn Asp
    840             845                 850

aac agc tgg atc cga cag cgc agt gcc agt gtc aac aaa gag cct gtt     3307
Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val
855             860                 865                 870

agt ctt cct ggg atc atg aga aga ggc gaa tct tta gat aac ctg gac     3355
Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp
                875             880                 885

tcc ccc cga tcc aat tct tgg aga cag cct cct tgg ctc aat cag ccc     3403
Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro
                890             895                 900

aca gga ttc tat gct tct tcc tct gtg caa gac ttt agt cgc cca cca     3451
Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln Asp Phe Ser Arg Pro Pro
            905             910                 915

cct cag ctg gtg tcc aca tca aac cgt gcc tac atg cgg aac ccc tcc     3499
Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser
    920             925                 930

tcc agc gtg ccc cca cct tca gct ggc tcc gtg aag acc tcc acc aca     3547
Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val Lys Thr Ser Thr Thr
935             940                 945                 950

ggt gtg gcc acc aca cag tcc ccc acc ccg aga agc cat tcc cct tca     3595
Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg Ser His Ser Pro Ser
                955             960                 965

gct tca cag tca ggc tct cag ctg cgt aac agg tca gtc agt ggg aag     3643
Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg Ser Val Ser Gly Lys
            970             975                 980

cgc ata tgc tcc tac tgc aat aac att ctg ggc aaa gga gcc gcc atg     3691
Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly Lys Gly Ala Ala Met
        985             990                 995

atc atc gag tcc ctg ggt ctt tgt tat cat ttg cat tgt ttt aag tgt     3739
Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu His Cys Phe Lys Cys
    1000            1005                1010

gtt gcc tgt gag tgt gac ctc gga ggc tct tcc tca gga gct gaa gtc     3787
Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser Ser Gly Ala Glu Val
1015            1020                1025                1030

agg atc aga aac cac caa ctg tac tgc aac gac tgc tat ctc aga ttc     3835
Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe
                1035                1040                1045
```

```
aaa tct gga cgg cca acc gcc atg tga tgtaagcctc catacgaaag          3882
Lys Ser Gly Arg Pro Thr Ala Met  *
            1050

cactgttgca gatagaagaa gaggtggttg ctgctcatgt agatctataa atatgtgttg   3942
tatgtctttt ttgctttttt tttaaaaaaa agaataactt tttttgcctc tttagattac   4002
atagaagcat tgtagtcttg gtagaaccag tattttttgtt gtttatttat aaggtaattg   4062
tgtgtgggga aaagtgcagt atttacctgt tgaattcagc atcttgagag cacaagggaa   4122
aaaataagaa cctacgaata tttttgaggc agataatgat ctagtttgac tttctagtta   4182
gtggtgtttt gaagagggta ttttattgtt ttttaaaaaa aggttcttaa acattatttg   4242
aaatagttaa tataaataca taattgcatt tgctctgttt attgtaatgt attctaaatt   4302
aatgcagaac catatggaaa atttcattaa aatctatccc caaatgtgct ttctgtatcc   4362
ttccttctac ctattattct gatttttaaa aatgcagtta atgtaccatt tatttgcttg   4422
atgaagggag ctctattttc tttaccagaa atgttgctaa gtaattccca atagaaagct   4482
gcttattttc attaatgaaa aataaccatg gtttgtatac tagaagtctt cttcagaaac   4542
tggtgagcct ttctgttcaa ttgcatttgt aaataaactt gctgatgcat ttaaaaaaaa   4602
aaaaaaaaaa                                                         4612


<210> 2
<211> 1054
<212> PRT
<213> Homo Sapiens

<400> 2
Met Gln Asp Tyr Asn Lys Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala
 1               5                   10                  15
Val Glu Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys
             20                  25                  30
Ser Arg Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro
             35                  40                  45
Asp Lys His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr
         50                  55                  60
Glu Ala Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser
65                   70                  75                  80
Ala Glu Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln
                 85                  90                  95
Lys Ile Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp
                100                 105                 110
Leu Ala Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln
            115                 120                 125
Lys Lys Lys Glu Glu Arg Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys
    130                 135                 140
Ser Lys Arg Ser Ser Lys Thr Phe Lys Glu Met Leu Gln Asp Arg Glu
145                 150                 155                 160
Ser Gln Asn Gln Lys Ser Thr Val Pro Ser Arg Arg Arg Met Tyr Ser
                165                 170                 175
Phe Asp Asp Val Leu Glu Glu Gly Lys Arg Pro Pro Thr Met Thr Val
                180                 185                 190
Ser Glu Ala Ser Tyr Gln Ser Glu Arg Val Glu Glu Lys Gly Ala Thr
            195                 200                 205
Tyr Pro Ser Glu Ile Pro Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg
```

```
            210                 215                 220
Glu Asp Arg Val Thr Thr Glu Ile Gln Leu Pro Ser Gln Ser Pro Val
225                 230                 235                 240
Glu Glu Gln Ser Pro Ala Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr
                245                 250                 255
Gln Met Glu Ser Thr Arg Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg
                260                 265                 270
Lys Thr Asp Thr Val Arg Leu Thr Ser Val Val Thr Pro Arg Pro Phe
                275                 280                 285
Gly Ser Gln Thr Arg Gly Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met
    290                 295                 300
Asp Asp Ala Trp Lys Tyr Asn Gly Asp Val Glu Asp Ile Lys Arg Thr
305                 310                 315                 320
Pro Asn Asn Val Val Ser Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln
                325                 330                 335
Leu Ala Ser Ser Leu Ser Ser Gln Lys Glu Val Ala Ala Thr Glu Glu
                340                 345                 350
Asp Val Thr Arg Leu Pro Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser
                355                 360                 365
Gln Asp Gln Ala Ala Thr Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly
    370                 375                 380
Leu Asp Leu Met Ser Glu Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg
385                 390                 395                 400
Glu Val Ser Arg Ser Gln Asp Gln Phe Ser Asp Met Arg Ile Ser Ile
                405                 410                 415
Asn Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp
                420                 425                 430
Asp Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala Gly Ser Pro Ala
                435                 440                 445
Glu Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile Ala Ile Asn Asn
    450                 455                 460
Thr Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu Glu Ala Met Ala
465                 470                 475                 480
Lys Ala Gln Glu Thr Gly His Leu Val Met Asp Val Arg Arg Tyr Gly
                485                 490                 495
Lys Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile
                500                 505                 510
Tyr Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr Thr Asp Phe Ser
    515                 520                 525
Glu Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile
    530                 535                 540
His Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser
545                 550                 555                 560
Leu Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser
                565                 570                 575
Asp Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile Ser Ala Pro Ser
    580                 585                 590
Arg Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp
    595                 600                 605
Gln Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln
    610                 615                 620
```

-8-

```
Glu Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg
625             630             635             640
Glu Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val Leu Ser Ser Asn
            645             650             655
Ser Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala
            660             665             670
Thr Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala
            675             680             685
Gly Glu Glu Glu Arg Arg Gln Pro Gln Glu Glu Val Val His Glu Asp
    690             695             700
Gln Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu Arg Glu Arg Lys
705             710             715             720
Trp Glu Gln Gln Leu Gln Glu Glu Gln Gln Lys Arg Leu Gln Ala
            725             730             735
Glu Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala
            740             745             750
Glu Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro
            755             760             765
Val Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe
    770             775             780
Leu Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp
785             790             795             800
Tyr Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly
            805             810             815
Asn Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu Gln Val Pro Ser
            820             825             830
Gly Ala Glu Leu Glu Arg Gln Gln Ile Leu Gln Glu Met Arg Lys Arg
            835             840             845
Thr Pro Leu His Asn Asp Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser
    850             855             860
Val Asn Lys Glu Pro Val Ser Leu Pro Gly Ile Met Arg Arg Gly Glu
865             870             875             880
Ser Leu Asp Asn Leu Asp Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro
            885             890             895
Pro Trp Leu Asn Gln Pro Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln
            900             905             910
Asp Phe Ser Arg Pro Pro Pro Gln Leu Val Ser Thr Ser Asn Arg Ala
            915             920             925
Tyr Met Arg Asn Pro Ser Ser Ser Val Pro Pro Pro Ser Ala Gly Ser
    930             935             940
Val Lys Thr Ser Thr Thr Gly Val Ala Thr Thr Gln Ser Pro Thr Pro
945             950             955             960
Arg Ser His Ser Pro Ser Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn
            965             970             975
Arg Ser Val Ser Gly Lys Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu
            980             985             990
Gly Lys Gly Ala Ala Met Ile Ile Glu Ser Leu Gly Leu Cys Tyr His
    995             1000            1005
Leu His Cys Phe Lys Cys Val Ala Cys Glu Cys Asp Leu Gly Gly Ser
    1010            1015            1020
Ser Ser Gly Ala Glu Val Arg Ile Arg Asn His Gln Leu Tyr Cys Asn
```

```
1025                   1030                   1035                   1040
Asp Cys Tyr Leu Arg Phe Lys Ser Gly Arg Pro Thr Ala Met
                  1045                   1050


<210> 3
<211> 4642
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (698)...(3892)

<400> 3
atagcacgac tgtgtatgct ctggaggact gaaaggctgt acaagcccta tgtatttttt     60
ttcaaatata catatgcatg ggtcttgctg ctgcctcttt tgctgactgt aattggactt    120
tgaagcttcg aagttatatc ataaaaattt gtaacctttg tctgagagag agctcagcta    180
agcaatcact ttccacttct tttcacagga taatataaac gttttcttga aagcttgtga    240
acagattgga ttgaaagaag cccagctttt ccatcctgga gatctacagg atttatcaaa    300
tcgagtcact gtcaagcaag aagagactga caggagagtg aaaaatgttt tgataacatt    360
gtactggctg ggaagaaaag cacaaagcaa cccgtactat aatggtcccc atcttaattt    420
gaaagcgttt gagaatcttt taggacaagc actgacgaag gcactcgaag actccagctt    480
cctgaaaaga agtggcaggg acagtggcta cggtgacatc tggtgtcctg aacgtggaga    540
atttcttgct cctccaaggc accataagag agaagattcc tttgaaagct tggactcttt    600
gggctcgagg tcattgacaa gctgctcctc tgatatcacg ttgagagggg ggcgtgaagg    660
ttttgaaagt gacacagatt cggaatttac attcaag atg cag gat tat aat aaa    715
                                          Met Gln Asp Tyr Asn Lys
                                            1              5

gat gat atg tcg tat cga agg att tcg gct gtt gag cca aag act gcg    763
Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu Pro Lys Thr Ala
            10              15              20

tta ccc ttc aat cgt ttt tta ccc aac aaa agt aga cag cca tcc tat    811
Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg Gln Pro Ser Tyr
        25              30              35

gta cca gca cct ctg aga aag aaa aag cca gac aaa cat gag gat aac    859
Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys His Glu Asp Asn
    40              45              50

aga aga agt tgg gca agc ccg gtt tat aca gaa gca gat gga aca ttt    907
Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala Asp Gly Thr Phe
55              60              65              70

tca aga ctc ttt caa aag att tat ggt gag aat ggg agt aag tcc atg    955
Ser Arg Leu Phe Gln Lys Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met
                75              80              85

agt gat gtc agc gca gaa gat gtt caa aac ttg cgt cag ctg cgt tac   1003
Ser Asp Val Ser Ala Glu Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr
```

-10-

```
gag gag atg cag aaa ata aaa tca caa tta aaa gaa caa gat cag aaa    1051
Glu Glu Met Gln Lys Ile Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys
        105             110                 115

tgg cag gat gac ctt gca aaa tgg aaa gat cgt cga aaa agt tac act    1099
Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr
    120             125                 130

tca gat ctg cag aag aaa aaa gaa gag aga gaa gaa att gaa aag cag    1147
Ser Asp Leu Gln Lys Lys Lys Glu Glu Arg Glu Glu Ile Glu Lys Gln
135             140                 145                 150

gca ctt gag aag tct aag aga agc tct aag acg ttt aag gaa atg ctg    1195
Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys Thr Phe Lys Glu Met Leu
            155                 160                 165

cag gac agg gaa tcc caa aat caa aag tct aca gtt ccg tca aga agg    1243
Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser Thr Val Pro Ser Arg Arg
            170                 175                 180

aga atg tat tct ttt gat gat gtg ctg gag gaa gga aag cga ccc cct    1291
Arg Met Tyr Ser Phe Asp Asp Val Leu Glu Glu Gly Lys Arg Pro Pro
        185                 190                 195

aca atg act gtg tca gaa gca agt tac cag agt gag aga gta gaa gag    1339
Thr Met Thr Val Ser Glu Ala Ser Tyr Gln Ser Glu Arg Val Glu Glu
        200                 205                 210

aag gga gca act tat cct tca gaa att ccc aaa gaa gat tct acc act    1387
Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro Lys Glu Asp Ser Thr Thr
215                 220                 225                 230

ttt gca aaa aga gag gac cgt gta aca act gaa att cag ctt cct tct    1435
Phe Ala Lys Arg Glu Asp Arg Val Thr Thr Glu Ile Gln Leu Pro Ser
            235                 240                 245

caa agt cct gtg gaa gaa caa agc cca gcc tct ttg tct tct ctg cgt    1483
Gln Ser Pro Val Glu Glu Gln Ser Pro Ala Ser Leu Ser Ser Leu Arg
            250                 255                 260

tca cgg agc aca caa atg gaa tca act cgt gtt tca gct tct ctc ccc    1531
Ser Arg Ser Thr Gln Met Glu Ser Thr Arg Val Ser Ala Ser Leu Pro
            265                 270                 275

aga agt tac cgg aaa act gat aca gtc agg tta aca tct gtg gtc aca    1579
Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg Leu Thr Ser Val Val Thr
        280                 285                 290

cca aga ccc ttt ggc tct cag aca agg gga atc tca tca ctc ccc aga    1627
```

```
Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly Ile Ser Ser Leu Pro Arg
295             300             305             310

tct tac acg atg gat gat gct tgg aag tat aat gga gat gtt gaa gac     1675
Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr Asn Gly Asp Val Glu Asp
            315             320             325

att aag aga act cca aac aat gtg gtc agc acc cct gca cca agc ccg     1723
Ile Lys Arg Thr Pro Asn Asn Val Val Ser Thr Pro Ala Pro Ser Pro
            330             335             340

gac gca agc caa ctg gct tca agc tta tct agc cag aaa gag gta gca     1771
Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser Ser Gln Lys Glu Val Ala
            345             350             355

gca aca gaa gaa gat gtg aca agg ctg ccc tct cct aca tcc ccc ttc     1819
Ala Thr Glu Glu Asp Val Thr Arg Leu Pro Ser Pro Thr Ser Pro Phe
            360             365             370

tca tct ctt tcc caa gac cag gct gcc act tct aaa gcc aca ttg tct     1867
Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr Ser Lys Ala Thr Leu Ser
375             380             385             390

tcc aca tct ggt ctt gat tta atg tct gaa tct gga gaa ggg gaa atc     1915
Ser Thr Ser Gly Leu Asp Leu Met Ser Glu Ser Gly Glu Gly Glu Ile
            395             400             405

tcc cca caa aga gaa gtc tca aga tcc cag gat cag ttc agt gat atg     1963
Ser Pro Gln Arg Glu Val Ser Arg Ser Gln Asp Gln Phe Ser Asp Met
            410             415             420

aga atc agc ata aac cag acg cct ggg aag agt ctt gac ttt ggg ttt     2011
Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe
            425             430             435

aca ata aaa tgg gat att cct ggg atc ttc gta gca tca gtt gaa gca     2059
Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala
            440             445             450

ggt agc cca gca gaa ttt tct cag cta caa gta gat gat gaa att att     2107
Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile
455             460             465             470

gct att aac aac acc aag ttt tca tat aac gat tca aaa gag tgg gag     2155
Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu
            475             480             485

gaa gcc atg gct aag gct caa gaa act gga cac cta gtg atg gat gtg     2203
Glu Ala Met Ala Lys Ala Gln Glu Thr Gly His Leu Val Met Asp Val
            490             495             500
```

```
agg cgc tat gga aag gct ggt tca cct gaa aca aag tgg att gat gca      2251
Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala
        505             510             515

act tct gga att tac aac tca gaa aaa tct tca aat cta tct gta aca      2299
Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr
        520             525             530

act gat ttc tcc gaa agc ctt cag agt tct aat att gaa tcc aaa gaa      2347
Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu
535             540             545             550

atc aat gga att cat gat gaa agc aat gct ttt gaa tca aaa gca tct      2395
Ile Asn Gly Ile His Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser
            555             560             565

gaa tcc att tct ttg aaa aac tta aaa agg cga tca caa ttt ttt gaa      2443
Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu
            570             575             580

caa gga agc tct gat tcg gtg gtt cct gat ctt cca gtt cca acc atc      2491
Gln Gly Ser Ser Asp Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile
        585             590             595

agt gcc ccg agt cgc tgg gtg tgg gat caa gag gag gag cgg aag cgg      2539
Ser Ala Pro Ser Arg Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg
        600             605             610

cag gag agg tgg cag aag gag cag gac cgc cta ctg cag gaa aaa tat      2587
Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr
615             620             625             630

caa cgt gag cag gag aaa ctg agg gaa gag tgg caa agg gcc aaa cag      2635
Gln Arg Glu Gln Glu Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln
            635             640             645

gag gca gag aga gag aat tcc aag tac ttg gat gag gaa ctg atg gtc      2683
Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val
            650             655             660

cta agc tca aac agc atg tct ctg acc aca cgg gag ccc tct ctt gcc      2731
Leu Ser Ser Asn Ser Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala
            665             670             675

acc tgg gaa gct acc tgg agt gaa ggg tcc aag tct tca gac aga gaa      2779
Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu
        680             685             690

gga acc cga gca gga gaa gag gag agg aga cag cca caa gag gaa gtt      2827
Gly Thr Arg Ala Gly Glu Glu Glu Arg Arg Gln Pro Gln Glu Glu Val
695             700             705             710
```

```
gtt cat gag gac caa gga aag aag ccg cag gat cag ctt gtt att gag      2875
Val His Glu Asp Gln Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu
                715                 720                 725


aga gag agg aaa tgg gag caa cag ctt cag gaa gag caa gag caa aag      2923
Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys
                730                 735                 740


cgg ctt cag gct gag gct gag gag cag aag cgt cct gcg gag gag cag      2971
Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln
                745                 750                 755


aag cgc cag gca gag ata gag cgg gaa aca tca gtc aga ata tac cag      3019
Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln
                760                 765                 770


tac agg agg cct gtt gat tcc tat gat ata cca aag aca gaa gaa gca      3067
Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala
775                 780                 785                 790


tct tca ggt ttt ctt cct ggt gac agg aat aaa tcc aga tct act act      3115
Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr
                795                 800                 805


gaa ctg gat gat tac tcc aca aat aaa aat gga aac aat aaa tat tta      3163
Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu
                810                 815              ←  820


gac caa att ggg aac acg acc tct tca cag agg aga tcc aag aaa gaa      3211
Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu
                825                 830                 835


caa gta cca tca gga gca gaa ttg gag agg caa caa atc ctt cag gaa      3259
Gln Val Pro Ser Gly Ala Glu Leu Glu Arg Gln Gln Ile Leu Gln Glu
                840                 845                 850


atg agg aag aga aca ccc ctt cac aat gac aac agc tgg atc cga cag      3307
Met Arg Lys Arg Thr Pro Leu His Asn Asp Asn Ser Trp Ile Arg Gln
855                 860                 865                 870


cgc agt gcc agt gtc aac aaa gag cct gtt agt ctt cct ggg atc atg      3355
Arg Ser Ala Ser Val Asn Lys Glu Pro Val Ser Leu Pro Gly Ile Met
                875                 880                 885


aga aga ggc gaa tct tta gat aac ctg gac tcc ccc cga tcc aat tct      3403
Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp Ser Pro Arg Ser Asn Ser
                890                 895                 900


tgg aga cag cct cct tgg ctc aat cag ccc aca gga ttc tat gct tct      3451
Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro Thr Gly Phe Tyr Ala Ser
```

-14-

```
tcc tct gtg caa gac ttt agt cgc cca cca cct cag ctg gtg tcc aca      3499
Ser Ser Val Gln Asp Phe Ser Arg Pro Pro Pro Gln Leu Val Ser Thr
        920              925              930

tca aac cgt gcc tac atg cgg aac ccc tcc tcc agc gtg ccc cca cct      3547
Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser Ser Ser Val Pro Pro Pro
935              940              945              950

tca gct ggc tcc gtg aag acc tcc acc aca ggt gtg gcc acc aca cag      3595
Ser Ala Gly Ser Val Lys Thr Ser Thr Thr Gly Val Ala Thr Thr Gln
            955              960              965

tcc ccc acc ccg aga agc cat tcc cct tca gct tca cag tca ggc tct      3643
Ser Pro Thr Pro Arg Ser His Ser Pro Ser Ala Ser Gln Ser Gly Ser
            970              975              980

cag ctg cgt aac agg tca gtc agt ggg aag cgc ata tgc tcc tac tgc      3691
Gln Leu Arg Asn Arg Ser Val Ser Gly Lys Arg Ile Cys Ser Tyr Cys
        985              990              995

aat aac att ctg ggc aaa gga gcc gcc atg atc atc gag tcc ctg ggt      3739
Asn Asn Ile Leu Gly Lys Gly Ala Ala Met Ile Ile Glu Ser Leu Gly
    1000             1005             1010

ctt tgt tat cat ttg cat tgt ttt aag tgt gtt gcc tgt gag tgt gac      3787
Leu Cys Tyr His Leu His Cys Phe Lys Cys Val Ala Cys Glu Cys Asp
1015             1020             1025             1030

ctc gga ggc tct tcc tca gga gct gaa gtc agg atc aga aac cac caa      3835
Leu Gly Gly Ser Ser Ser Gly Ala Glu Val Arg Ile Arg Asn His Gln
            1035             1040             1045

ctg tac tgc aac gac tgc tat ctc aga ttc aaa tct gga cgg cca acc      3883
Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe Lys Ser Gly Arg Pro Thr
            1050             1055             1060

gcc atg tga tgtaagcctc catacgaaag cactgttgca gatagaagaa              3932
Ala Met  *
```

```
gaggtggttg ctgctcatgt agatctataa atatgtgttg tatgtctttt ttgctttttt    3992
tttaaaaaaa agaataactt tttttgcctc tttagattac atagaagcat tgtagtcttg    4052
gtagaaccag tattttttgtt gtttatttat aaggtaattg tgtgtgggga aaagtgcagt    4112
atttacctgt tgaattcagc atcttgagag cacaagggaa aaaataagaa cctacgaata    4172
ttttttgaggc agataatgat ctagtttgac tttctagtta gtggtgtttt gaagagggta    4232
ttttattgtt ttttaaaaaa aggttcttaa acattatttg aaatagttaa tataaataca    4292
taattgcatt tgctctgttt attgtaatgt attctaaatt aatgcagaac catatggaaa    4352
atttcattaa aatctatccc caaatgtgct ttctgtatcc ttccttctac ctattattct    4412
gattttttaaa aatgcagtta atgtaccatt tatttgcttg atgaagggag ctctattttc    4472
```

-15-

```
tttaccagaa atgttgctaa gtaattccca atagaaagct gcttattttc attaatgaaa    4532
aataaccatg gtttgtatac tagaagtctt cttcagaaac tggtgagcct ttctgttcaa    4592
ttgcatttgt aaataaactt gctgatgcat ttaaaaaaaa aaaaaaaaa                 4642
```

<210> 4
<211> 1064
<212> PRT
<213> Homo Sapiens

<400> 4
```
Met Gln Asp Tyr Asn Lys Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala
 1               5                  10                  15
Val Glu Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys
                20                  25                  30
Ser Arg Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro
            35                  40                  45
Asp Lys His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr
        50                  55                  60
Glu Ala Asp Gly Thr Phe Ser Arg Leu Phe Gln Lys Ile Tyr Gly Glu
65                  70                  75                  80
Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu Asp Val Gln Asn
                85                  90                  95
Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile Lys Ser Gln Leu
                100                 105                 110
Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp
            115                 120                 125
Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys Lys Lys Glu Glu Arg
        130                 135                 140
Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys
145                 150                 155                 160
Thr Phe Lys Glu Met Leu Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser
                165                 170                 175
Thr Val Pro Ser Arg Arg Arg Met Tyr Ser Phe Asp Asp Val Leu Glu
                180                 185                 190
Glu Gly Lys Arg Pro Pro Thr Met Thr Val Ser Glu Ala Ser Tyr Gln
            195                 200                 205
Ser Glu Arg Val Glu Glu Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro
        210                 215                 220
Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg Glu Asp Arg Val Thr Thr
225                 230                 235                 240
Glu Ile Gln Leu Pro Ser Gln Ser Pro Val Glu Glu Gln Ser Pro Ala
                245                 250                 255
Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr Gln Met Glu Ser Thr Arg
                260                 265                 270
Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg
            275                 280                 285
Leu Thr Ser Val Val Thr Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly
        290                 295                 300
Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr
305                 310                 315                 320
Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro Asn Asn Val Val Ser
```

```
                        325                     330                     335
Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser
                340                 345                 350
Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp Val Thr Arg Leu Pro
        355                 360                 365
Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr
    370                 375                 380
Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu Asp Leu Met Ser Glu
385                 390                 395                 400
Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu Val Ser Arg Ser Gln
                405                 410                 415
Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys
            420                 425                 430
Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe
        435                 440                 445
Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln
    450                 455                 460
Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn
465                 470                 475                 480
Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly
            485                 490                 495
His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu
        500                 505                 510
Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser
        515                 520                 525
Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser
    530                 535                 540
Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His Asp Glu Ser Asn Ala
545                 550                 555                 560
Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg
            565                 570                 575
Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp Ser Val Val Pro Asp
            580                 585                 590
Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg Trp Val Trp Asp Gln
        595                 600                 605
Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg
        610                 615                 620
Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu Lys Leu Arg Glu Glu
625                 630                 635                 640
Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu
            645                 650                 655
Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser Met Ser Leu Thr Thr
            660                 665                 670
Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser
        675                 680                 685
Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly Glu Glu Glu Arg Arg
        690                 695                 700
Gln Pro Gln Glu Glu Val Val His Glu Asp Gln Gly Lys Lys Pro Gln
705                 710                 715                 720
Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln
            725                 730                 735
```

```
Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys
            740                 745                 750
Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr
            755                 760                 765
Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile
            770                 775                 780
Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn
785                     790                 795                 800
Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn
                    805                 810                 815
Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln
                820                 825                 830
Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly Ala Glu Leu Glu Arg
            835                 840                 845
Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr Pro Leu His Asn Asp
    850                 855                 860
Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val
865                 870                 875                 880
Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp
                885                 890                 895
Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro
            900                 905                 910
Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln Asp Phe Ser Arg Pro Pro
            915                 920                 925
Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser
    930                 935                 940
Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val Lys Thr Ser Thr Thr
945                 950                 955                 960
Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg Ser His Ser Pro Ser
            965                 970                 975
Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg Ser Val Ser Gly Lys
            980                 985                 990
Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly Lys Gly Ala Ala Met
            995                 1000                1005
Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu His Cys Phe Lys Cys
    1010                1015                1020
Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser Ser Gly Ala Glu Val
1025                1030                1035                1040
Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe
                1045                1050                1055
Lys Ser Gly Arg Pro Thr Ala Met
                1060
```

<210> 5
<211> 549
<212> DNA
<213> Homo Sapiens

<400> 5
gcaccataag agagaagatt cctttgaaag cttggactct ttgggctcga ggtcattgac   60
aagctgctcc tctgatatca cgttgagagg ggggcgtgaa ggttttgaaa gtgacacaga   120

-18-

```
ttcggaattt acattcaaga tgcaggatta taataaagat gatatgtcgt atcgaaggat      180
ttcggctgtt gagccaaaga ctgcgttacc cttcaatcgt tttttaccca acaaaagtag      240
acagccatcc tatgtaccag cacctctgag aaagaaaaag ccagacaaac atgaggataa      300
cagaagaagt tgggcaagcc cggtttatac agaagcagat ggaacatttt caagactctt      360
tcaaaagatt tatggtgaga atgggagtaa gtccatgagt gatgtcagcg cagaagatgt      420
tcaaaacttg cgtcagctgc gttacgagga gatgcagaaa ataaaatcac aattaaaaga      480
acaagatcag aaatggcagg atgaccttgc aaagtggaaa gatcgtcgaa aaagttacac      540
ttcagatct                                                             549
```

```
<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
gtaacttttt cgacgatctt tccac                                            25


<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
tattttctgc atctcctcgt aacgc                                            25


<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
tgacatcact catggactta ctccc                                            25


<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
```

gttccatctg cttctgtata aaccg   25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
tctgttatcc tcatgtttgt ctggc   25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
tctggctttt tctttctcaa agtgc   25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
aagtgctggt acatagatgg ctgtc   25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
tctacttttg ttggggttga aaacg   25

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
tgtgtcactt tcaaaaactt cacgc   25

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
agagcagctt gtctatgaac tccag   25

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
cgggaaatcg tgcgtgacat taag   24

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
tgatctcctt ctgcatcctg tcgg   24

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ttcgtagcat cagttgaagc agg   23

<210> 19

(

```
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
ggtgaaccag cctttccata gc                                                    22
```